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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/618,941	07/15/2003	David Whyte	034536-0321	6608

22428 7590 01/24/2006

FOLEY AND LARDNER LLP
SUITE 500
3000 K STREET NW
WASHINGTON, DC 20007

EXAMINER	
MONSHIPOURI, MARYAM	
ART UNIT	**PAPER NUMBER**
1653	

DATE MAILED: 01/24/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/618,941	WHYTE ET AL.	
	Examiner	Art Unit	
	Maryam Monshipouri	1653	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on _____.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) 1-36 is/are pending in the application.

4a) Of the above claim(s) 6-25 and 30-36 is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) 1-5 and 26-29 is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: see attachment

Applicant's response to restriction requirement filed 12/9/2005 is acknowledged. Applicant elected Group I (claims 1-5, 26-29, SEQ ID NO99 only) with traverse. In traversal of restriction requirement applicant argues that the requirement to elect a single sequence runs counter to the PTO's own policy that "up to ten (10) independent and distinct nucleotide sequences will be examined in a single application without restriction," to aid biotechnology industry "without creating an undue burden on the Office". According to applicant the Office has failed to articulate any justification for suspending that policy in this case. In view of applicant the Office has not established that the sequences in this application are any more difficult to examine than those in a " biotechnology case " thereby making it unreasonable to examine more than a single sequence. Accordingly, applicant request withdrawal and revision of the restriction requirement.

These arguments wren fully considered but were found **unpersuasive** for the following reasons: Firstly the examiner respectfully disagrees with the applicant that electing a single sequence runs counter to the office policy. This is because said policy does not bar examining a single invention in a single application. Secondly, said policy does not specify that distinct sequences are directed to patentably distinct inventions. The major restriction criteria applied to this instant invention is based on patentably distinct inventions rather than patentably distinct sequences, which allows for an appropriate search and examination of each invention leading to issuance of valid patents which in its turn aids the biotechnology industry much more than incompletely searching many patentably distinct inventions in a single application. Applicant is well

aware of the exponential growth of commercially available sequence databases since the time of establishment of said policy i.e. 11/1996, and she/he can surely appreciate that searching any additional sequences (inventions) in the instant databases does requires many hours of additional sequence searching as well as key word searching, which **does impose an undue burden** of searching on the examiner and is not even required by the criteria set forth in 35 USC section 121.

Therefore, in view of arguments provided above and in view of MPEP criteria set forth for restriction shown in the previous office action, the examiner finds no reason to withdraw the restriction requirement, which is now **Final.**

DETAILED ACTION

Claims 1-5, 26-29, (SEQ ID NO:99 only) are under examination on the merits. Claims 6-25, 30-36 and SEQ ID NO:67-98, 100-132 are withdrawn as drawn to non-elected invention.

Claim Objections

Claims 1-5, 26-29 are objected to because of the following informalities: said claims still recite non-elected subject matter, namely SEQ ID NO:67-98, 100-132. Applicant is advised to delete non-elected subject matter from said claims. Appropriate correction is required.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-5 and 28-29 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The phrases " N-terminal domain", "C-terminal catalytic domain", "C-terminal domain" etc. in claim 1 and its dependent claims 2-5, 28 - 29 are unclear. In page 22 some of these terms have been defined. However, for example, it is unclear whether "N-terminal region" and "N-terminal domain" are identical or different. Further even if one assumes that said terms are identical the definition provided is non-specific to the instant invention. Again looking at the definition of "N-terminal region", it is unclear where the catalytic domain of SEQ ID NO:99 starts and where exactly in between the initiator methionine and catalytic domain applicant is referring to. These problems also exist with all the other terms recited in claim 1. Appropriate clarification is required.

Claims 1-5, 28-29 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claim 1 as recited requires that all parts (a)-(d) encode kinases by recitation of activity in the preamble. Thus, it is believed that recitation of activity in claim 1(c) is redundant. Further, if one assumes that the function in the preamble may be applied to parts (a)-(e) of claim 1 it s unclear how a polypeitde that lacks catalytic domain (see part (d)) can retain kinase function.

Claims 2-5 and 28-29 are merely rejected for depending from are rejected base claim 1.

Claims 2 and 29 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. In claim 2 applicant is claiming the nucleic acid of claim 1 comprising a vector while in claim 29 he/she is claiming a vector comprising the same nucleic acid. It is unclear if in both claims vectors are identical structures or different. Appropriate clarification is required.

Claims 26-27 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The term "consisting essentially of " in claims 26-27 is confusing. In page 254 applicant has defined said term as to be replaceable by "consisting of" or comprising" and refers to said terms as terms of description and not limitation. As applicant is well aware MPEP interprets the term "consisting essentially of" as open language and said term can only be replaced by "comprising" and not by "consisting of" which is closed language and is a limiting term. Hence, for examination purposes "consisting essentially of" is assumed to have the same meaning as "comprising". Appropriate clarification is required.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 26-27 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for isolated nucleic acids having SEQ ID NO:33 or

encoding SEQ ID NO:99, does not reasonably provide enablement for any isolated nucleic consisting essentially of 10-30 bases of a sequence encoding SEQ ID NO:99 or consisting essentially of 10-30 bases of SEQ ID NO:33.

The criteria for undue experimentation, summarized in *re Wands*, 8, USPQ2n 1400 (Fed. Cir. 1988) are: 1) the quantity of experimentation necessary, 2) the amount of direction or guidance presented, 3) the presence and absence of working examples, 4) the nature of the invention, 5) the state of prior art, 6) the relative skill of those in the art, 7) the predictability or unpredictability of the art, and 8) the breadth of the claims.

The specification fails to teach which additional residues beyond the 10-30 bases defined in claimed probes is in charge of assigning kinase function to said products. No examples of such residues are provided either. Current state of the art indicates that for nucleic acid probe to retain any function it must at least encode the catalytic region. Such region in the case of kinases is typically 250-300 amino acids long, which requires a nucleic acid length of 750-900 contiguous bases.

Therefore, due to lack of sufficient information and examples provided in the specification and due to unpredictability of prior art as to which residues beyond the 10-30 contiguous residues of SEQ ID NO:33 or those encoding SEQ ID NO:99 should be retained in the claimed probes such that they encode kinases one of skill in the art has to go through the burden of undue experimentation in order to screen for those probes that are within the scope of this invention and as such the claims are not fully enabled.

Claims 26-27 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter

which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. Claims 26-27 are each direct to a **genus** of nucleic acids that have not been adequately described in the specification.

The specification does not contain any disclosure of the function of all DNA sequences that are consisting essentially of 10-30 contiguous residues of SEQ ID NO:33 or are consisting essentially of 10-30 residues of a DNA sequence encoding SEQ ID NO:99. The genus of cDNAs that consists essentially of these above cDNA molecules is a large variable genus with the potentiality of encoding many different proteins. Therefore, many functionally unrelated DNAs are encompassed within the scope of these claims, including partial DNA sequences. The specification discloses only a **single species** of each claimed genus (DNA encoding SEQ ID NO:99 and SEQ ID NO:33) which is insufficient to put one of skill in the art in possession of the attributes and features of all species within the claimed genus. Therefore, one skilled in the art cannot reasonably conclude that the applicant had possession of the claimed invention at the time the instant application was filed.

Applicant is referred to the revised interim guidelines concerning compliance with the written description requirement of U.S.C. 112, first paragraph, published in the Official Gazette and also available at www.uspto.gov.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

Claims 1-5, 26-29 are rejected under 35 U.S.C. 102(e) as being anticipated by Furness et al. (U.S. patent No. 6,673,549, issued 1/2004). Furness teaches a human DNA sequence (see its SEQ ID NO:1053) which inherently encodes a kinase product having 97.8% identity to SEQ ID NO:99 of this invention and its sequence does hybridize to the DNA sequence encoding SEQ ID NO:99 under stringent conditions (see the attached sequence alignment) anticipating claims 1, 4-5 and consists essentially of 10-30 contiguous nucleotides of SEQ ID NO:33 or that encoding SEQ ID NO:99 anticipating claims 26-27. In columns 17-18, Furness teaches about vectors and host cells comprising its DNA sequences anticipating claims 2-3 and 28-29.

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1-5, 26-29 are rejected under 35 U.S.C. 102(b) as being anticipated by Plowman et al. (WO200073469, 12/2000). Plowman teaches a DNA sequence (see its SEQ ID NO:61) that encodes a human kinase and hybridizes to a DNA sequence (see the attached sequence alignment) encoding SEQ ID NO:99 under stringent conditions, anticipating claims 1, 4-5. Its sequence consists essentially of 10-30 residues of SEQ ID NO:33 or that encoding SEQ ID NO:99 anticipating claims 26-27. In pages 32-35, Plowman teaches about vectors and host cells comprising its DNA sequences anticipating claims 2-3 and 28-29.

No claims are allowed.

Allowable Subject Matter

Isolated DNA sequences encoding SEQ ID NO:99 or comprising SEQ ID NO:33 are free of prior art. Further, the prior art does not teach or suggest preparing such specifically claimed DNA sequences. Hence said sequences are also non-obvious.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Maryam Monshipouri whose telephone number is (571) 272-0932. The examiner can normally be reached on 7:00 a.m to 4:30 p.m. except for alternate Mondays.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Weber Jon P. can be reached on (571) 272-0925. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Maryam Monshipouri Ph.D.

Primary Examiner

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 13, 2006, 21:25:25 ; Search time 255 Seconds
(without alignments)
3534.211 Million cell updates/sec

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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2612	97.8	4048	3	US-09-976-594-1053	Sequence 1053, Ap
2	1617	60.6	981	3	US-09-345-473E-9	Sequence 9, Appli
3	1617	60.6	981	3	US-09-862-027-9	Sequence 9, Appli
4	1534.5	57.5	2029	2	US-08-933-750C-69	Sequence 69, Appl
5	1534.5	57.5	2029	3	US-09-234-613-69	Sequence 69, Appl
6	1534.5	57.5	2163	3	US-09-949-016-1428	Sequence 1428, Ap
7	1508.5	56.5	2241	3	US-09-023-942A-9	Sequence 9, Appli
8	490.5	18.4	2546	3	US-10-104-047-1939	Sequence 1939, Ap
9	413.5	15.5	17616	3	US-09-949-016-13170	Sequence 13170, A
10	383.5	14.4	669	3	US-09-040-984-23	Sequence 23, Appl
11	383.5	14.4	669	3	US-09-123-912-23	Sequence 23, Appl
12	383.5	14.4	669	3	US-09-643-597-23	Sequence 23, Appl
13	383.5	14.4	669	3	US-09-480-884A-23	Sequence 23, Appl
14	383.5	14.4	669	3	US-09-542-615A-23	Sequence 23, Appl
15	383.5	14.4	669	3	US-09-606-421B-23	Sequence 23, Appl
16	383.5	14.4	669	3	US-09-221-107-23	Sequence 23, Appl
17	383.5	14.4	669	3	US-09-466-396A-23	Sequence 23, Appl
18	383.5	14.4	669	3	US-09-476-496A-23	Sequence 23, Appl
19	383.5	14.4	669	3	US-09-630-940B-23	Sequence 23, Appl
20	383.5	14.4	669	3	US-09-285-479-23	Sequence 23, Appl
21	383.5	14.4	669	3	US-10-007-700-23	Sequence 23, Appl
22	383	14.3	260	3	US-09-016-434-978	Sequence 978, App
23	364.5	13.7	334	3	US-09-270-767-104	Sequence 104, App
24	364.5	13.7	334	3	US-09-270-767-15386	Sequence 15386, A
25	359.5	13.5	2226	3	US-09-854-856-59	Sequence 59, Appl
26	359.5	13.5	2226	3	US-10-010-720-59	Sequence 59, Appl
27	359.5	13.5	2310	3	US-09-854-856-43	Sequence 43, Appl
28	359.5	13.5	2310	3	US-10-010-720-43	Sequence 43, Appl
29	359.5	13.5	2406	3	US-09-854-856-27	Sequence 27, Appl
30	359.5	13.5	2406	3	US-10-010-720-27	Sequence 27, Appl
31	359.5	13.5	2490	3	US-09-854-856-11	Sequence 11, Appl
32	359.5	13.5	2490	3	US-10-010-720-11	Sequence 11, Appl
33	359.5	13.5	2685	3	US-09-854-856-53	Sequence 53, Appl
34	359.5	13.5	2685	3	US-10-010-720-53	Sequence 53, Appl
35	359.5	13.5	2769	3	US-09-854-856-37	Sequence 37, Appl
36	359.5	13.5	2769	3	US-10-010-720-37	Sequence 37, Appl
37	359.5	13.5	2865	3	US-09-854-856-21	Sequence 21, Appl
38	359.5	13.5	2865	3	US-10-010-720-21	Sequence 21, Appl
39	359.5	13.5	2949	3	US-09-854-856-5	Sequence 5, Appli
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45	359.5	13.5	5916	3	US-09-854-856-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-09-976-594-1053
; Sequence 1053, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 1053
; LENGTH: 4048
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 399133.9
US-09-976-594-1053

Alignment Scores:

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Percent Similarity:	98.62%	Conservative:	0
Best Local Similarity:	98.62%	Mismatches:	0
Query Match:	97.83%	Indels:	7
DB:	3	Gaps:	1

US-10-618-941-99 (1-507) x US-09-976-594-1053 (1-4048)

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Qy         21 GluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArgTrpGlnLysArg 40
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Qy         61 ThrGluGluGlyValGluValValTrpAsnGluLeuHisPheGlyAspArgLysAlaPhe 80
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Qy         81 AlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValLeuValAspHisPro 100
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Qy        101 AsnIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAlaCysAlaArgValIle 120
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Qy        121 PheIleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLysLysThrLysLys 140
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Qy        141 AsnHisLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysThrGlnIleLeuSerAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        702 AACCACAAGGCCATGAACGCCCGGGCCTGGAAGCGCTGGTGCACGCAGATCCTGTCTGCG 761

Qy        161 LeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLeuThrSerAspThr 180
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Db        762 CTCAGCTTCCTGCACGCCTGCAGCCCCCCAATCATCCACGGGAACCTGACCAGCGACACC 821

Qy        181 IlePheIleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHisArgIlePheSer 200
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Db        822 ATCTTCATTCAGCACAACGGCCTCATCAAGATCGGCTCCGTGTGGCACCGAATCTTCTCC 881

Qy        201 AsnAlaLeuArgProProThrAlaLeuProAspAspLeuArgSerProIleArgAlaGlu 220
              |||                 ||||||||||||||||||||||||||||||||||||||||||||
Db        882 AAT-----------------GCACTTCCAGATGATCTCCGAAGCCCCATCCGCGCTGAG 923

Qy        221 ArgGluGluLeuArgAsnLeuHisPhePheProProGluTyrGlyGluValAlaAspGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        924 CGAGAGGAACTTCGGAACCTGCACTTCTTCCCCCCAGAGTATGGAGAGGTGGCCGATGGG 983

Qy        241 ThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMetAlaValLeuGluIle 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        984 ACCGCTGTGGACATCTTCTCCTTTGGGATGTGTGCGCTGGAGATGGCTGTACTGGAAATC 1043

Qy        261 GlnThrAsnGlyAspThrArgValThrGluGluAlaIleAlaArgAlaArgHisSerLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1044 CAGACCAATGGGGACACCCGGGTCACAGAGGAGGCCATTGCTCGCGCCAGGCACTCGCTG 1103

Qy        281 SerAspProAsnMetArgGluPheIleLeuCysCysLeuAlaArgAspProAlaArgArg 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1104 AGTGACCCCAACATGCGGGAGTTCATCCTTTGCTGCCTGGCCCGGGACCCTGCCCGCCGG 1163

Qy        301 ProSerAlaHisSerLeuLeuPheHisArgValLeuPheGluValHisSerLeuLysLeu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1164 CCCTCTGCCCACAGCCTCCTCTTCCACCGCGTGCTCTTCGAGGTGCACTCGCTGAAGCTC 1223

Qy        321 LeuAlaAlaHisCysPheIleGlnHisGlnTyrLeuMetProGluAsnValValGluGlu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1224 CTGGCAGCCCACTGCTTCATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTGGAGGAG 1283

Qy        341 LysThrLysAlaMetAspLeuHisAlaValLeuAlaGluLeuProArgProArgArgPro 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1284 AAGACCAAGGCCATGGACCTGCACGCGGTCTTGGCGGAGCTTCCCCGGCCCCGCAGGCCC 1343

Qy        361 ProLeuGlnTrpArgTyrSerGluValSerPheMetGluLeuAspLysPheLeuGluAsp 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1344 CCGCTGCAGTGGCGGTACTCGGAAGTCTCCTTCATGGAGCTGGACAAATTCCTGGAGGAT 1403

Qy        381 ValArgAsnGlyIleTyrProLeuMetAsnPheAlaAlaThrArgProLeuGlyLeuPro 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1404 GTCAGGAATGGAATCTACCCACTGATGAACTTTGCAGCCACTCGACCCCTGGGGCTGCCC 1463

Qy        401 ArgValLeuAlaProProProGluGluValGlnLysAlaLysThr-ProThrProGluPr 420
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       1464 CGTGTGCTGGCCCCACCCCCGGAGGAGGTCCAAAAGGCCAAGACCCCCGACGCCAGAGCC 1523

Qy        420 oPheAspSerGluThrArgLysValIleGlnMetGlnCysAsnLeuGluArgSerGluAs 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1524 CTTTGACTCTGAGACCAGAAAGGTCATCCAGATGCAGTGCAACCTGGAGAGAAGCGAGGA 1583

Qy        440 pLysAlaArgTrpHisLeuThrLeuLeuLeuValLeuGluAspArgLeuHisArgGlnLe 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1584 CAAGGCGCGCTGGCATCTCACTCTGCTTCTGGTGCTGGAAGACCGGCTGCACCGGCAGCT 1643

Qy        460 uThrTyrAspLeuLeuProThrAspSerAlaGlnAspLeuAlaSerGluLeuValHisTy 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1644 GACCTACGACCTGCTCCCAACGGACAGCGCCCAGGACCTCGCCTCGGAGCTCGTGCACTA 1703

Qy        480 rGlyPheLeuHisGluAspAspArgMetLysLeuAlaAlaPheLeuGluSerThrPheLe 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1704 TGGCTTCCTCCACGAGGACGACCGGATGAAGCTGGCCGCCTTCCTGGAGAGCACCTTCCT 1763

Qy        500 uLysTyrArgGlyThrGlnAla 507
              |||||||||||||||||||||
Db       1764 CAAGTACCGTGGGACCCAGGCC 1785
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RESULT 2
US-09-345-473E-9
; Sequence 9, Application US/09345473E
; Patent No. 6558903
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin
; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof
; FILE REFERENCE: 35800/183781
; CURRENT APPLICATION NUMBER: US/09/345,473E
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(981)
; OTHER INFORMATION: n = A,T,C or G
US-09-345-473E-9

Alignment Scores:

Pred. No.:	2.52e-169	Length:	981
Score:	1617.00	Matches:	312
Percent Similarity:	96.89%	Conservative:	0
Best Local Similarity:	96.89%	Mismatches:	3
Query Match:	60.56%	Indels:	7
DB:	3	Gaps:	1

US-10-618-941-99 (1-507) x US-09-345-473E-9 (1-981)

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Qy          1 MetAlaAlaProGluProAlaProArgArgAlaArgGluArgGluArgGluArgGluAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         35 ATGGCGGCCCCGGAGCCGGCGCCGAGGCGGGCCCGGGAACGGGAGCGGGAGCGGGAGGAC 94

Qy         21 GluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArgTrpGlnLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 GAGAGCGAGGACGAGAGCGACATCCTGGAGGAAAGCCCGTGTGGTCGCTGGCAAAAGCGA 154

Qy         41 ArgGluGlnValAsnGlnGlyAsnMetProGlyLeuGlnSerThrPheLeuAlaMetAsp 60
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Db       1369 GAAGACCGGCTGCACCGGCAGCTGACCTACGAGCTGCTCCCAACGGACAGCGCCCAGGAC 1428

Qy        473 LeuAlaSerGluLeuValHisTyrGlyPheLeuHisGlu----------AspAspArg 488

Db       1429 CTCGCCTCGGAGCTCGTGCACTATGGCTTCCTCCACGAGGTGCGCTGGGCGGACGACCGG 1488

Qy        489 MetLysLeuAlaAlaPheLeuGluSerThrPheLeuLysTyrArgGlyThrGlnAla 507

Db       1489 ATGAAGCTGGCCGCCTTCCTGGAGAGCACCTTCCTCAAGTACCGTGGGACCCAGGCC 1545
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RESULT 4
AX056416

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LOCUS       AX056416                3304 bp    DNA     linear   PAT 13-JAN-2001
DEFINITION  Sequence 60 from Patent WO0073469.
ACCESSION   AX056416
VERSION     AX056416.1  GI:12229123
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Plowman,G.D., Martinez,R., Whyte,D. and Sudersanam,S.
  TITLE     Protein kinases
  JOURNAL   Patent: WO 0073469-A 60 07-DEC-2000;
            Sugen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .3304
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:          2.3e-196    Length:          3304
Score:              2409.00     Matches:         460
Percent Similarity: 98.72%      Conservative:    2
Best Local Similarity: 98.29%   Mismatches:      0
Query Match:        90.22%      Indels:          6
DB:                 6           Gaps:            1

US-10-618-941-99 (1-507) x AX056416 (1-3304)

Qy         40 ArgArgGluGlnValAsnGlnGlyAsnMetProGlyLeuGlnSerThrPheLeuAlaMet 59

Db          1 CAGAGAGAGAAGGTAAACCAAGGGAACATGCCAGGGCTTCAGAGCACCTTCCTAGCCATG 60

Qy         60 AspThrGluGluGlyValGluValValTrpAsnGluLeuHisPheGlyAspArgLysAla 79

Db         61 GACACGGAGGAGGGGGTAGAGGTGGTGTGGAACGAGCTCCACTTCGGAGACAGGAAGGCC 120

Qy         80 PheAlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValLeuValAspHis 99

Db        121 TTCGCGGCGCACGAGGAGAAGATCCAGACCGTGTTCGAGCAGCTGGTGCTGGTGGACCAC 180

Qy        100 ProAsnIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAlaCysAlaArgVal 119

Db        181 CCGAACATCGTGAAGTTGCACAAGTACTGGCTGGATACCTCTGAGGCCTGCGCGAGGGTC 240

Qy        120 IlePheIleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLysLysThrLys 139

Db        241 ATCTTCATCACAGAGTACGTGTCATCAGGCAGCCTCAAGCAATTCCTCAAAAAGACCAAG 300

Qy        140 LysAsnHisLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysThrGlnIleLeuSer 159

Db        301 AAGAACCACAAGGCCATGAACGCCCGGGCCTGGAAGCGCTGGTGCACGCAGATCCTGTCT 360

Qy        160 AlaLeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLeuThrSerAsp 179

Db        361 GCGCTCAGCTTCCTGCACGCCTGCAGCCCCCAATCATCCACGGGAACCTGACCAGCGAC 420

Qy        180 ThrIlePheIleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHisArgIlePhe 199

Db        421 ACCATCTTCATTCAGCACAACGGCCTCATCAAGATCGGCTCCGTGTGGCACCGAATCTTC 480

Qy        200 SerAsnAlaLeuArgProProThrAlaLeuProAspAspLeuArgSerProIleArgAla 219

Db        481 TCCAAT----------GCACTTCCAGATGATCTCCGAAGCCCCATCCGCGCT 522

Qy        220 GluArgGluGluLeuArgAsnLeuHisPhePheProProGluTyrGlyGluValAlaAsp 239

Db        523 GAGCGAGAGGAACTTCGGAACCTGCACTTCTTCCCCCCAGAGTATGGAGAGGTGGCCGAT 582

Qy        240 GlyThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMetAlaValLeuGlu 259

Db        583 GGGACCGCTGTGGACATCTTCTCCTTTGGGATGTGTGCGCTGGAGATGGCTGTACTGGAA 642

Qy        260 IleGlnThrAsnGlyAspThrArgValThrGluGluAlaIleAlaArgAlaArgHisSer 279

Db        643 ATCCAGACCAATGGGGACACCCGGGTCACAGAGGAGGCCATTGCTCGCGCCAGGCACTCG 702

Qy        280 LeuSerAspProAsnMetArgGluPheIleLeuCysCysLeuAlaArgAspProAlaArg 299

Db        703 CTGAGTGACCCCAACATGCGGGAGTTCATCCTTTGCTGCCTGGCCCGGGACCCTGCCCGC 762

Qy        300 ArgProSerAlaHisSerLeuLeuPheHisArgValLeuPheGluValHisSerLeuLys 319

Db        763 CGGCCCTCTGCCCACAGCCTCCTCTTCCACCGCGTGCTCTTCGAGGTGCACTCGCTGAAG 822

Qy        320 LeuLeuAlaAlaHisCysPheIleGlnHisGlnTyrLeuMetProGluAsnValValGlu 339

Db        823 CTCCTGGCAGCCCACTGCTTCATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTGGAG 882

Qy        340 GluLysThrLysAlaMetAspLeuHisAlaValLeuAlaGluLeuProArgProArgArg 359

Db        883 GAGAAGACCAAGGCCATGGACCTGCACGCGGTCTTGGCGGAGCTTCCCCGGCCCCGCAGG 942

Qy        360 ProProLeuGlnTrpArgTyrSerGluValSerPheMetGluLeuAspLysPheLeuGlu 379

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Qy        380 AspValArgAsnGlyIleTyrProLeuMetAsnPheAlaAlaThrArgProLeuGlyLeu 399

Db       1003 GATGTCAGGAATGGAATCTACCCACTGATGAACTTTGCAGCCACTCGACCCCTGGGGCTG 1062

Qy        400 ProArgValLeuAlaProProProGluGluValGlnLysAlaLysThrProThrProGlu 419

Db       1063 CCCCGTGTGCTGGCCCCACCCCCGGAGGAGGTCCAAAAGGCCAAGACCCCGACGCCAGAG 1122

Qy        420 ProPheAspSerGluThrArgLysValIleGlnMetGlnCysAsnLeuGluArgSerGlu 439

Db       1123 CCCTTTGACTCTGAGACCAGAAAGGTCATCCAGATGCAGTGCAACCTGGAGAGAAGCGAG 1182

Qy        440 AspLysAlaArgTrpHisLeuThrLeuLeuLeuValLeuGluAspArgLeuHisArgGln 459

Db       1183 GACAAGGCGCGCTGGCATCTCACTCTGCTTCTGGTGCTGGAAGACCGGCTGCACCGGCAG 1242

Qy        460 LeuThrTyrAspLeuLeuProThrAspSerAlaGlnAspLeuAlaSerGluLeuValHis 479

Db       1243 CTGACCTACGACCTGCTCCCAACGGACAGCGCCCAGGACCTCGCCTCGGAGCTCGTGCAC 1302

Qy        480 TyrGlyPheLeuHisGluAspAspArgMetLysLeuAlaAlaPheLeuGluSerThrPhe 499

Db       1303 TATGGCTTCCTCCACGAGGACGACCGGATGAAGCTGGCCGCCTTCCTGGAGAGCACCTTC 1362

Qy        500 LeuLysTyrArgGlyThrGlnAla 507

Db       1363 CTCAAGTACCGTGGGACCCAGGCC 1386
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RESULT 5
HSM801974

```
LOCUS       HSM801974               3538 bp    mRNA    linear   PRI 18-FEB-2000
DEFINITION  Homo sapiens mRNA; cDNA DKFZp434P086 (from clone DKFZp434P086);
            partial cds.
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